

RESULT 1

ALDX_SPOSA

ID ALDX_SPOSA STANDARD; PRT; 322 AA.
AC P27800; Q12707;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aldehyde reductase I (EC 1.1.1.2) (Alcohol dehydrogenase [NADP+])
DE (ALR).
GN ARI.
OS Sporobolomyces salmonicolor.
OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
OC Microbotryomycetidae; Sporidiobolales; Sporidiobolus.
OX NCBI_TaxID=5005;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 33-124; 132-153; 156-199 AND
RP 202-313, AND FUNCTION.
RC STRAIN=Aku 4429;
RX MEDLINE=96271678; PubMed=8779568;
RA Kita K., Matsuzaki K., Hashimoto T., Yanase H., Kato N.,
RA Chung M.C.-M., Kataoka M., Shimizu S.;
RT "Cloning of the aldehyde reductase gene from a red yeast,
RT Sporobolomyces salmonicolor, and characterization of the gene and its
RT product.";
RL Appl. Environ. Microbiol. 62:2303-2310(1996).
RN [2]
RP SEQUENCE OF 1-51, AND ENZYME REGULATION.
RC STRAIN=Aku 4429;
RX MEDLINE=92338224; PubMed=1633196;
RA Kataoka M., Sakai H., Morikawa T., Katoh M., Miyoshi T., Shimizu S.,
RA Yamada H.;
RT "Characterization of aldehyde reductase of Sporobolomyces
RT salmonicolor.";
RL Biochim. Biophys. Acta 1122:57-62(1992).
CC -!- FUNCTION: Catalyzes the asymmetric reduction of aliphatic and
CC aromatic aldehydes and ketones to an R-enantiomer. Reduces ethyl
CC 4-chloro-3-oxobutanoate to ethyl (R)-4-chloro-3-hydroxybutanoate.
CC -!- CATALYTIC ACTIVITY: An alcohol + NADP(+) = an aldehyde + NADPH.
CC -!- ENZYME REGULATION: Inhibited by quercetin, dicoumarol and some SH-
CC reagents.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.
CC -----
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CC -----
DR EMBL; U26463; AAB17362.1; -.
DR PIR; S78113; S78113.
DR HSSP; P15121; 2ACQ.
DR GO; GO:0005623; C:cell; IDA.
DR GO; GO:0008106; F:alcohol dehydrogenase (NADP) activity; IDA.
DR InterPro; IPR001395; Aldo/ket_red.

RESULT 2

US-10-040-416-6

; Sequence 6, Application US/10040416

; Publication No. US20020160480A1

; GENERAL INFORMATION:

; APPLICANT: OOKURA, TETUYA

; APPLICANT: KASUMI, TAKAFUMI

; APPLICANT: ASABA, EIJI

; TITLE OF INVENTION: ERYTHROSE REDUCTASE, ITS cDNA AND CELL WHICH THE cDNA
EXPRESS

; FILE REFERENCE: 217969US0XCIP

; CURRENT APPLICATION NUMBER: US/10/040,416

; CURRENT FILING DATE: 2002-01-09

; PRIOR APPLICATION NUMBER: US 09/800,487

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: JP 2001-001294

; PRIOR FILING DATE: 2001-01-09

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Trichosporonoides megachiliensis

US-10-040-416-6

Query Match 99.4%; Score 1697; DB 13; Length 328;
Best Local Similarity 99.4%; Pred. No. 2.8e-156;
Matches 326; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSYNKNIPLNDGNSIPALGYGTWQAEPGQVGEVKLAVKAGYRHLDLAKVYQNQTEIGQA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MSYNKNIPLNDGNSIPALGYGTWQAEPGQVGEVKLAVKAGYRHLDLAKVYQNQTEIGQA 60

Qy 61 LKELFDEGVVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LKELFDEGVVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKF 120

Qy 121 TTPDELLPADPTNKDLAYIDDSVKLSDTWKAVVALKKTGKTKSVGSNFSTRVLVDLVEEA 180
||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 TTPDELLPADPTNKDLAYVDDSVKLSDTWKAVVALKKTGKTKSVGSNFSTRVLVDLVEEA 180

Qy 181 SGERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNNVAGKPPLTENPGIVDAAKR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SGERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNNVAGKPPLTENPGIVDAAKR 240

Qy 241 LNHTPAAVLIAWGIQRGYSVLVSVTPSRIKSFEQITLSDEEFQRTNLIKEYGESRNN 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 LNHTPAAVLIAWGIQRGYSVLVSVTPSRIKSFEQITLSDEEFQRTNLIKEYGESRNN 300

Qy 301 VPFNYKPSWSIDVFGTQYEAKATHKINA 328
||| ||| ||| ||| ||| ||| ||| |||

Db 301 VPFNYKPSWSIDVFGTQDEAKATHKINA 328

Qy 243 HTPAAVLIAWGIQRGYSVLVKSVTPSRIKS NFEQITLSDEEFQRVTNLIKEYGESRNNVP 302
||| ||||| | |:||: ||||||| ||:||:|| |: | : | | | :|
Db 237 CTPAQVLIAWAIVGGSVIPKS VTPSRIGENFKQVSLSQEDVDAVSKLGE GS GR RRYNIP 296

Qy 303 FNYKPSWSIDVFGTQYEAKATHKI 326
| | | | :||| : | : :
Db 297 CTYSPKWDINVFGEEDEKSCKNAV 320